IN THE CLAIMS

Please cancel Claim 3 without prejudice to or disclaimer of the subject matter presented therein. Please amend Claims 2 and 10 as shown below.

1.   (Cancelled)

2.   (Currently Amended) A method for identifying a base sequence present in a target single-stranded nucleic acid comprising the steps of:

(a) preparing a probe array in which single-stranded nucleic acid probes of No. 1 to No. n (n≥3) are arranged as isolated spots on a substrate;

(b) reacting a single-stranded nucleic acid which has a base sequence fully complementary to a base sequence of one of the single-stranded nucleic acid probes and is fluorescence-labeled, with the probe array under such conditions that single-stranded nucleic acids complementary to each other form a double-stranded nucleic acid;

removing the unreacted labeled single-stranded nucleic acid; and

measuring fluorescence intensity of each spot of the probe array to obtain a first template pattern showing a relationship between location of the probes and fluorescent characteristics;

(c) analyzing the first template pattern to locate probes and to calculate a mean value of fluorescence intensities (F_i) of the double-stranded nucleic acids having i of mismatched base pairs, where i is an integer not less than 1;

(d) <u>determining a threshold value by</u> calculating a difference (F_1, 0) between

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a mean value of ~~a mean value of~~ the fluorescence ~~intensities~~ intensity of the fully complementary

double-stranded nucleic ~~acids~~ acid without mismatch (F0) and a mean value of

fluorescence intensities of double-stranded nucleic acids having one-base mismatch (F1),

and by further calculating a difference (Fi+1, i) between a mean value of fluorescence

intensities of a double-stranded nucleic acid having (i+1) base mismatches (Fi+1) and the

mean value of the fluorescence intensities of the double-stranded nucleic acids having

i-base mismatches (Fi), and identifying i being Fi+1, i << Fi, i-1, wherein the threshold

value is set between the mean value of the fluorescence intensities having i-base

mismatches (Fi) and the mean value of the fluorescence intensities having (i+1)

mismatches (Fi+1);

(e) preparing a second template pattern of positive probe spots of probes

having base sequences differing from the base sequence of the second probe by i or less

bases where i is determined in said step (d), wherein negative probe spots are probes having

base sequences differing from the second probe by more than i bases;

(f) performing the same operation as the step (e) for each of remaining

single-stranded nucleic acid probes and obtaining template patterns of No. 3 to No. n

showing a relationship between location and fluorescent characteristics of the probes;

(g) performing the same operation as the step (b) using a sample containing

the target single-stranded nucleic acid of the base sequence to obtain a sample pattern

showing a relationship between a position and fluorescent characteristics, wherein the

sample pattern is obtained by using the threshold value;

(h) comparing the sample pattern obtained in the step (g) with a plurality of

template patterns, the plurality of template patterns comprising the first and second

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template patterns and the template patterns of No. 3 to No. n, to find a template pattern

substantially identical to the sample pattern; and

(i) determining the base sequence of the target single-stranded nucleic acid

to be a base sequence complementary to the base sequence of the probe taken for the

preparation of the template pattern found in the step (h).

3.   (Cancelled)

4.   (Previously Presented) The method according to claim 2, wherein

the length of each of the single-stranded nucleic acid probes is 8 mer to 30 mer.

5.   (Previously Presented) The method according to claim 4, wherein

the length of each of the single-stranded nucleic acid probes is 12 mer to 25 mer.

6.   (Original) The method according to claim 2, wherein the number of

the mismatched base pairs (i) is 1.

7 to 9. (Cancelled)

10.   (Currently Amended) A method for identifying a base sequence

present in a target nucleic acid by using a DNA chip in which a plurality of probes are

arranged, comprising the steps of:

reacting a target nucleic acid which has a known base sequence and is

fluorescence-labeled, with the DNA chip and then observing the DNA chip after the reaction to obtain a template pattern showing a relationship between the probe location and the fluorescence intensity;

reacting a target nucleic acid which has an unknown base sequence and is fluorescence-labeled, with the DNA chip and then observing the DNA chip after the reaction to obtain a sample pattern showing a relationship between the probe location and the fluorescence intensity; and

comparing the sample pattern with the template pattern to thereby determine whether the unknown base sequence agrees with the known base sequence,

wherein a threshold value is ~~set up between a fluorescence intensity corresponding to i base mismatch(es) and a fluorescence intensity corresponding to i+1 base mismatches based on~~ <u>determined by calculating</u> a difference between a mean value of fluorescence intensities of i-base mismatches and a mean value of fluorescence intensities of i+1 mismatches, where i is an integer not less than 1, <u>and is set between the mean value of fluorescence intensities of i-base mismatches and the mean value of fluorescence intensities of i+1 mismatches,</u> such that a probe location showing a fluorescence intensity above the threshold value is defined to be positive while a probe location otherwise is defined to be negative, and the template pattern and the sample pattern are prepared by adopting only positive probe locations.

11.   (Previously Presented) The method according to claim 10, wherein i is 1.

REMARKS

Claims 2, 4 to 6, 10, and 11 are in the application, of which Claims 2 and 10 are independent. Claim 3 has been cancelled without prejudice. Claims 2 and 10 have been amended herein. Reconsideration and further examination are respectfully requested.

Entry of the January 3, 2007 Amendment After Final Rejection is respectfully requested. The changes made herein are in addition to the changes made in that Amendment.
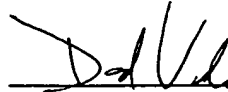
Claims 2 to 6, 10, and 11 were rejected under 35 U.S.C. § 102(e) over U.S. Patent No. 6,228,575 (Gingeras). The rejection is respectfully traversed.

Applicants wish to thank the Examiner for the courtesies extended to Applicants' undersigned representative during the personal interview conducted on March 8, 2007. During the interview, the Examiner tentatively indicated that he would be inclined to more favorably view the application if the claims were amended along the lines set forth above.

The application is believed to be in condition for allowance, and a Notice of Allowance is respectfully requested.

Applicants' undersigned attorney may be reached in our Costa Mesa, California office by telephone at (714) 540-8700. All correspondence should be directed to our address given below.

Respectfully submitted,

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